

S. Wegert



1600

RAW SEQUENCE LISTING

DATE: 04/17/2003

PATENT APPLICATION: US/09/679,687B

TIME: 12:02:56

Input Set : A:\BB1162 US NA Corrected Seq Listing.txt

Output Set: N:\CRF4\04172003\I679687B.raw

3 <110> APPLICANT: Allen, Stephen M.
 4 Hitz, William D.
 5 Rafalski, J. Antoni
 7 <120> TITLE OF INVENTION: SUCROSE TRANSPORT PROTEINS
 9 <130> FILE REFERENCE: BB1162 US NA
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/679,687B
 C--> 12 <141> CURRENT FILING DATE: 2001-03-05
 14 <150> PRIOR APPLICATION NUMBER: 60/081,148
 15 <151> PRIOR FILING DATE: 1998-04-09
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/07562
 18 <151> PRIOR FILING DATE: 1999-04-07
 20 <160> NUMBER OF SEQ ID NOS: 28
 22 <170> SOFTWARE: Microsoft Office 97
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2088
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Zea mays
 29 <400> SEQUENCE: 1

P.6

ENTERED

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32 atcgatccta gctagctagc tagctagggc gcgaccgtcg tctcggtggt tgttgacagg  180
33 tcccgtagct gtgtgctcgc catggctcgt ggcgacggcg ggcagctggc ggagctgtcc  240
34 gcgggggtcc gcggcgcggc cgcggtggtg gaccacgtgg ccccgatcag cctcgggagg  300
35 ctcatcctcg ccggcatggt cgccggcggc gtgcagtagc gctgggcgct gcagctctcc  360
36 ctccctcacgc cctacgtgca gactctgggg ctttcacatg cgctcacttc attcatgtgg  420
37 ctctgcggcc ctattgccgg cttagtggtc caaccgctgg ttggcctgta cagcgacagg  480
38 tgtacatcga gatgggggag acggaggccg tttatcctga cagggtgcat gctcatctgc  540
39 gttgccgtca ttgttgctcg attctcgtca gacatcggag ctgctctagg ggacacgaag  600
40 gaacactgca gcctctacca cggtcctcgt tggcacgctg cgatcgtgta cgttctgggg  660
41 ttttggtccc ttgacttctc caacaacact gtgcagggtc cagcacgtgc tatgatggct  720
42 gatctatgtg accatcatgg gccaaagtgc gctaactcca tcttctgttc ttggatggcg  780
43 ctgggaaaca tcctaggcta ctccctctggc tccacgaaca attggcacia gtggtttccc  840
44 ttccttaaaa cgagcgccgt ctgtgaggcc tgtgcgaacc tgaaagggtc atttctggtg  900
45 gccgtggtgt tcctagtcct gtgcctgacg gtaaccctga tcttcgcaa ggaggtgccg  960
46 tacagagcga acgagaacct cccgacgacg aaggccggcg gcgaggtcga gactgagcct 1020
47 accggggcac ttgccgtgct caagggtctc aaggacctgc ctcccgggat gccgtccgtg 1080
48 ctccctcgtg ctgccatcac ctggccttcg tgggtcccggt tcatcctcta cgacaccgac 1140
49 tggatgggccc gggagatcta ccacggcgac cccaagggga gcaacgccc gatctcggcg 1200
50 ttcaacgaag gtgtccgagt cggcgcgctt cgggtgctac tcaactcggg tattctaggg 1260
51 ttcagctcgt tcctgatcga gcccatgtgc gggaaggctg ggccgagggt ggtgtgggtg 1320
52 acgagcaact tcatggtctg cgtcgccatg gcggccaccg cgctgatcag cttctggctg 1380
53 ctgagggact accacgggta cgtgcaggac gccatcaccg cgaacgccag catcaaggcc 1440
54 gtctgcctcg tcctcttcgc cttcctgggc gtccctctcg ccatcctgta cagcgtcccg 1500
  
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55 ttcgcggtga cggcgcagct ggcggccacc cggggcggcg ggcaggggct gtgcaccggc 1560
56 gtcctcaaca tctccatcgt catccctcag gtgatcatcg cgctgggcgc cggcccgtgg 1620
57 gacgcgctgt tcgggaaggg caacatcccg gcgttcggcg tcgcgtcggc cttcgccctc 1680
58 gtcggcggcg tcgtgggcgt gttcctgctg cccaagatct ccaagcgcca gttccggggc 1740
59 gtcagcgcg ggcggccactg atcgaacccg gccggggccg gccgccggca cgcagcccgg 1800
60 caagagctgt atgttggtga gagttgaaca gaaaccatgc atgtgtgctt ctgtagttct 1860
61 gttgtttgtg gtcgatcgat gggcgttgcg tggcagcggt ggcaagcgag gcgaggtgcg 1920
62 cggatccaaa aaaagggcca ttcgatcaat caatgtgtag tagagtacaa ctagacgatg 1980
63 atgttcacat catttgtctt taatacatac cggtttctat tgtctttaaa aaaaaaaaaa 2040
64 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2088
66 <210> SEQ ID NO: 2
67 <211> LENGTH: 519
68 <212> TYPE: PRT
69 <213> ORGANISM: Zea mays
71 <400> SEQUENCE: 2
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73 1 5 10 15
75 Arg Gly Ala Ala Ala Val Val Asp His Val Ala Pro Ile Ser Leu Gly
76 20 25 30
78 Arg Leu Ile Leu Ala Gly Met Val Ala Gly Gly Val Gln Tyr Gly Trp
79 35 40 45
81 Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln Thr Leu Gly Leu
82 50 55 60
84 Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly Pro Ile Ala Gly
85 65 70 75 80
87 Leu Val Val Gln Pro Leu Val Gly Leu Tyr Ser Asp Arg Cys Thr Ser
88 85 90 95
90 Arg Trp Gly Arg Arg Arg Pro Phe Ile Leu Thr Gly Cys Met Leu Ile
91 100 105 110
93 Cys Val Ala Val Ile Val Val Gly Phe Ser Ser Asp Ile Gly Ala Ala
94 115 120 125
96 Leu Gly Asp Thr Lys Glu His Cys Ser Leu Tyr His Gly Pro Arg Trp
97 130 135 140
99 His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe Ser
100 145 150 155 160
102 Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Met Met Ala Asp Leu Cys
103 165 170 175
105 Asp His His Gly Pro Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp Met
106 180 185 190
108 Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser Thr Asn Asn Trp
109 195 200 205
111 His Lys Trp Phe Pro Phe Leu Lys Thr Ser Ala Cys Cys Glu Ala Cys
112 210 215 220
114 Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Val Phe Leu Val Leu
115 225 230 235 240
117 Cys Leu Thr Val Thr Leu Ile Phe Ala Lys Glu Val Pro Tyr Arg Ala
118 245 250 255
120 Asn Glu Asn Leu Pro Thr Thr Lys Ala Gly Gly Glu Val Glu Thr Glu
121 260 265 270

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123 Pro Thr Gly Pro Leu Ala Val Leu Lys Gly Phe Lys Asp Leu Pro Pro
124      275      280      285
126 Gly Met Pro Ser Val Leu Leu Val Thr Ala Ile Thr Trp Leu Ser Trp
127      290      295      300
129 Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr
130 305      310      315      320
132 His Gly Asp Pro Lys Gly Ser Asn Ala Gln Ile Ser Ala Phe Asn Glu
133      325      330      335
135 Gly Val Arg Val Gly Ala Phe Gly Leu Leu Asn Ser Val Ile Leu
136      340      345      350
138 Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Arg Lys Val Gly Pro
139      355      360      365
141 Arg Val Val Trp Val Thr Ser Asn Phe Met Val Cys Val Ala Met Ala
142      370      375      380
144 Ala Thr Ala Leu Ile Ser Phe Trp Ser Leu Arg Asp Tyr His Gly Tyr
145 385      390      395      400
147 Val Gln Asp Ala Ile Thr Ala Asn Ala Ser Ile Lys Ala Val Cys Leu
148      405      410      415
150 Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu Tyr Ser Val
151      420      425      430
153 Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Thr Arg Gly Gly Gly Gln
154      435      440      445
156 Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile Pro Gln Val
157      450      455      460
159 Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Ala Leu Phe Gly Lys Gly
160 465      470      475      480
162 Asn Ile Pro Ala Phe Gly Val Ala Ser Ala Phe Ala Leu Val Gly Gly
163      485      490      495
165 Val Val Gly Val Phe Leu Leu Pro Lys Ile Ser Lys Arg Gln Phe Arg
166      500      505      510
168 Ala Val Ser Ala Gly Gly His
169      515

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171 <210> SEQ ID NO: 3

172 <211> LENGTH: 825

173 <212> TYPE: DNA

174 <213> ORGANISM: Zea mays

176 <400> SEQUENCE: 3

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178 ggcaataaaa acagtcaaga tcacggcatt ggttgttttc tctcttctcg gattgccact 120
179 ctccatcact tacagcgttc cgttttctgt gactgctgag ctgactgccg gtacaggagg 180
180 tggacaaggt ttggccacag gagtcctaaa tcttgctatc gtggttcccc agatagtagt 240
181 gtcgcttggg gcaggtccat gggacgctct gtatggagga ggaataccc cggcgttcgt 300
182 cttggcttcg gtcttctccc tggcagcagc tgtgctcgca gttctcaagc tgccaaagct 360
183 gtccaaactg taccaatctg ccgggttcca tggattggc tgatgctcat gcccaaaaca 420
184 ccccgtctg ccatgtaaaa catcacacca acatttgcc ccattttgcc attcgtttac 480
185 agagaaatga ttcttttttc ctctgtacaac tacagaataa tgacagtga agtaggagtt 540
186 taggtgagag agagagagag gctaggtagg ttgatgtgaa ggtgtaaaag ctgtatcctc 600
187 ctttttttgt ttttgttttt gtttttgaca gtgtatgtaa gagctgtcca caagaaaatt 660
188 tacaagtggg gtaacctgcc ctctgttgta cattgtacta ctactacatg acaatcatat 720

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189 gtcctttgtc tttatccaag gttgaagacg taaactgagg ccatctatctt atcttgggcc 780
190 atgaaaaaaaa aaaaaaaaaa aaaaaaaact cgaaactagt tctct 825
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193 <211> LENGTH: 133
194 <212> TYPE: PRT
195 <213> ORGANISM: Zea mays
197 <400> SEQUENCE: 4
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199 1 5 10 15
201 His Ile Ile Gly Ala Asn Lys Thr Val Lys Ile Thr Ala Leu Val Val
202 20 25 30
204 Phe Ser Leu Leu Gly Leu Pro Leu Ser Ile Thr Tyr Ser Val Pro Phe
205 35 40 45
207 Ser Val Thr Ala Glu Leu Thr Ala Gly Thr Gly Gly Gly Gln Gly Leu
208 50 55 60
210 Ala Thr Gly Val Leu Asn Leu Ala Ile Val Val Pro Gln Ile Val Val
211 65 70 75 80
213 Ser Leu Gly Ala Gly Pro Trp Asp Ala Leu Tyr Gly Gly Gly Asn Thr
214 85 90 95
216 Pro Ala Phe Val Leu Ala Ser Val Phe Ser Leu Ala Ala Gly Val Leu
217 100 105 110
219 Ala Val Leu Lys Leu Pro Lys Leu Ser Asn Ser Tyr Gln Ser Ala Gly
220 115 120 125
222 Phe His Gly Phe Gly
223 130
225 <210> SEQ ID NO: 5
226 <211> LENGTH: 1977
227 <212> TYPE: DNA
228 <213> ORGANISM: Zea mays
230 <400> SEQUENCE: 5
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232 ggcgcgcgtgc agtacggctg ggcgctgcag ctctccctcc tcacgcccta cgtgcagact 120
233 ctggggctct cactatgccct cacttcattc atgtggctat gcggtcctat tgctggctta 180
234 gtggtccaac cgctgggttg cctgtacagc gatagggtgca cagcaagatg gggaagacgc 240
235 aggccattta tctgatagg atgcatgctc atctgccttg ccgtcattgt tgttggcttc 300
236 tcgtccgaca tcggagctgc tctaggggac acaaaggaac actgcagcct ctaccacggc 360
237 cctcgtttgg atgctgcgat cgtgtacgtt ctggggtttt ggctccttga cttctccaac 420
238 aatactgtgc aagggtccagc gcgtgctatg atggctgatc tgtgcggtca tcatgggcct 480
239 agtgcagcca actcaatctt ctgttcttgg atggcgctgg gaaacatcct aggctattcc 540
240 tctggctcca caaacaactg gcacaagtgg ttcccggttc ttatgacaaa cgcgtgctgt 600
241 gaagcctgcg caaacctgaa aggcgcgttt ctggtggctg tgggtgttct aatcatgtgc 660
242 ttgactataa ccctgttctt cgccaaggaa gtgccctaca gaggaacca gaacctcccc 720
243 acaaaggcaa acggcgaggt cgagactgaa ccttcgggcc cactcgtgt gctcaagggc 780
244 tccaagaact tgcccacggg gatgccgtcc gtgctcctcg taactggact cacctggctc 840
245 tcttggttcc cgttcattct ctacgacacc gactggatgg gccgtgagat ctaccacggc 900
246 gaccccaagg gtagcaacgc tcagatctcg gcgttcgacg aaggcgtcag agttggctcg 960
247 ttcgggctgc tgctcaactc gatcgttcta ggattcagct cgttcctgat cgagcccatg 1020
248 tgccggaagg tcgggccgag ggtggtgtgg gtgacgagca acttcatggg ctgcgtcgcc 1080
249 atggcgcca ccgcgctgat cagcttctgg tcgctcaagg actaccacgg atacgtgcag 1140

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250 gacgccatca cgcgcagcac gagcatcaag gccgtctgcc tcgtcctctt cgcgttcctg 1200
251 ggtgtcccctc tcgccatcct gtacagcgtc ccgttcgcgg tgacggcgca gctggcgggc 1260
252 acgaagggcg gcgggcaggg gctgtgcacc ggcgtgctca acatctccat cgtcatccct 1320
253 caggtgatca tcgcgctggg cgcggggccc tgggacgcgc tgttcggcaa gggcaacatc 1380
254 ccggcgttcg gcgtggcgtc ggggttcgcc ctcatcggcg gcgtcgtggg cgtgttcctg 1440
255 ctgcccaga tctccaagcg ccagttccgc gccgtcagcg cgggcggcca ctgatcgcg 1500
256 ccgcccgcgc ggagcacggc acggcggcac agcccagccg tgctagagct gtatgttttg 1560
257 aaagttgaaa cagaataaga agcgggcgaa acgagaaaac catgcatgtc atgtgtgtgc 1620
258 ttttgttgtg tgtggggtgg ggcaagcgag gcgaggtgtg tggaggtgaa gtgaaggtga 1680
259 gcatatccag caccagctgg taccaaggtc gggctctctg gctagtgtta ttagctagt 1740
260 taaggagcga gtaggtcagt taaggctggg gcgtcgtgag ggctgtcttg tgtgtagcta 1800
261 cagcagacgg ttcatacagaa ggattattcg tgcagtatat acagtacaac tagacaatga 1860
262 tgttgatgat tggcttagag ctagaggcct atagccctat actactgtgt attgtccgcc 1920
263 gttttagttt tttggtccca tcccatcaat gcaaccgcct tgttttaaaa aaaaaaa 1977
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 497
267 <212> TYPE: PRT
268 <213> ORGANISM: Zea mays
270 <400> SEQUENCE: 6
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274 Gly Met Val Ala Gly Gly Val Gln Tyr Gly Trp Ala Leu Gln Leu Ser
275 20 25 30
277 Leu Leu Thr Pro Tyr Val Gln Thr Leu Gly Leu Ser His Ala Leu Thr
278 35 40 45
280 Ser Phe Met Trp Leu Cys Gly Pro Ile Ala Gly Leu Val Val Gln Pro
281 50 55 60
283 Leu Val Gly Leu Tyr Ser Asp Arg Cys Thr Ala Arg Trp Gly Arg Arg
284 65 70 75 80
286 Arg Pro Phe Ile Leu Ile Gly Cys Met Leu Ile Cys Leu Ala Val Ile
287 85 90 95
289 Val Val Gly Phe Ser Ser Asp Ile Gly Ala Ala Leu Gly Asp Thr Lys
290 100 105 110
292 Glu His Cys Ser Leu Tyr His Gly Pro Arg Trp His Ala Ala Ile Val
293 115 120 125
295 Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe Ser Asn Asn Thr Val Gln
296 130 135 140
298 Gly Pro Ala Arg Ala Met Met Ala Asp Leu Cys Gly His His Gly Pro
299 145 150 155 160
301 Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp Met Ala Leu Gly Asn Ile
302 165 170 175
304 Leu Gly Tyr Ser Ser Gly Ser Thr Asn Asn Trp His Lys Trp Phe Pro
305 180 185 190
307 Phe Leu Met Thr Asn Ala Cys Cys Glu Ala Cys Ala Asn Leu Lys Gly
308 195 200 205
310 Ala Phe Leu Val Ala Val Val Phe Leu Ile Met Cys Leu Thr Ile Thr
311 210 215 220
313 Leu Phe Phe Ala Lys Glu Val Pro Tyr Arg Gly Asn Gln Asn Leu Pro
314 225 230 235 240

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 1007
Seq#:14; Xaa Pos. 311,321
Seq#:19; N Pos. 1093